

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M. Ruben

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SmithKline Beecham Corporation
- (B) STREET: 709 Swedeland Road
- (C) CITY: King of Prussia
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/018,961
- (B) FILING DATE: 05 JUNE 1996

- (A) APPLICATION NUMBER: 60/020,344
- (B) FILING DATE: 23 MAY 1996

- (A) APPLICATION NUMBER: 60/017,949
- (B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Han, William T.
 (B) REGISTRATION NUMBER: 34,344
 (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5219
 (B) TELEFAX: 610-270-5090
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
 1 5 10 15
 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
 20 25 30
 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
 35 40 45
 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
 50 55 60
 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
 65 70 75 80
 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
 85 90 95
 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
 100 105 110
 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
 115 120 125
 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
 130 135 140

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG 60
 CTGCAGGTGG ACTAGCTCTG GGACGTCTCTG CTGAGCCGCG AGCTGTTTCTG GCCCCATATG 120
 ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCGGCGGG ATCAGGCCAG GCAGCTGATC 180
 ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCTTTTGT TCATCTCCTG CTTAGAGGAC 240
 ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCTG 300
 AAGCCAACCC TAGAAAACCT TACCCAGTG GTGCTCAGAC CAGAGATTCG CAAACCAGAG 360
 GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT CTGGAGGATT CCGTGATGTC 420
 GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC 480
 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC 540
 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTT 600
 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG 660
 GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG TCATTCTCTC TCACGGCTGT 720
 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCTG 780
 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC 840
 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC 900
 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC 960
 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT 1020
 GACATCTTTG TGTCTACTC TACTTTCCCA GGTTTTGTTC CCTGGAGGGA CCCCAGAGT 1080
 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC 1140
 CTGCAGTCCC TCCTGCTTAG GGTGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG 1200
 ATGCCTGGTT GCTTTAATTT CCTCCGAAA AAACCTTTTCT TTAACATC ATAAGGCCAG 1260
 GGCCCCCTAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG 1320
 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT 1380
 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT 1440
 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT 1500
 CCAGGGCTAG TGAATTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA 1560
 CCTCTGCACT ACTGACAT 1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| CTGACTGCCA | AGAAAATGGT | GCTGGCTTTG | CTGGAGCTGG | CGCGGCAGGA | CCACGGTGCT | 60 |
| CTGGACTGCT | GCGTGGTGGT | CATTCCTCTCT | CACGGCTGTC | AGGCCAGCCA | CCTGCAGTTC | 120 |
| CCAGGGGCTG | TCTACGGCAC | AGATGGATGC | CCTGTGTCGG | TCGAAAAGAT | TGTGAACATC | 180 |
| TTCAATGGGA | CCAGCTGCCC | CAGCCTGGGA | GGGAAGCCCA | AGCTCTTTTTT | CATCCAGGCC | 240 |
| TGTGGTGGGG | AGCAGAAAGA | CCATGGGTTC | GAGGTGGCCT | CCACTTCCCC | TGAAGACGAG | 300 |
| TCCCCTGGCA | GTAACCCCGA | GCCAGATGCC | ACCCCGTTCC | AGGAAGGTTT | GAGGACCTTC | 360 |
| GACCAGCTGG | ACGCCATATC | TAGTTTGCCC | ACACCCAGTG | ACATCTTTGT | GTCCCTACTCT | 420 |
| ACTTTCCCAG | GTTTTGTTTC | CTGGAGGGAC | CCCAAGAGTG | GCTCCTGGTA | CGTTGAGACC | 480 |
| CTGGACGACA | TCTTTGAGCA | GTGGGCTCAC | TCTGAAGACC | TGCAGTCCCT | CCTGCTTAGG | 540 |
| GTCGCTAATG | CTGTTTCGGT | GAAAGGGATT | TATAAACAGA | TGCCTGGTTG | CTTTAATTTT | 600 |
| CTCCGGAAAA | AACTTTTCTT | TTAAAACATC | ATAAGGCAG | | | 639 |

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- 68 -

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | 70 | | 75 | | 80 | | | | | | | | | |
| Lys | Asp | His | Gly | Phe | Glu | Val | Ala | Ser | Thr | Ser | Pro | Glu | Asp | Glu | Ser |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Pro | Gly | Ser | Asn | Pro | Glu | Pro | Asp | Ala | Thr | Pro | Phe | Gln | Glu | Gly | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Thr | Phe | Asp | Gln | Leu | Asp | Ala | Ile | Ser | Ser | Leu | Pro | Thr | Pro | Ser |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asp | Ile | Phe | Val | Ser | Tyr | Ser | Thr | Phe | Pro | Gly | Phe | Val | Ser | Trp | Arg |
| | 130 | | | | | | 135 | | | | 140 | | | | |
| Asp | Pro | Lys | Ser | Gly | Ser | Trp | Tyr | Val | Glu | Thr | Leu | Asp | Asp | Ile | Phe |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Glu | Gln | Trp | Ala | His | Ser | Glu | Asp | Leu | Gln | Ser | Leu | Leu | Leu | Arg | Val |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Ala | Asn | Ala | Val | Ser | Val | Lys | Gly | Ile | Tyr | Lys | Gln | Met | Pro | Gly | Cys |
| | | 180 | | | | | | 185 | | | | | | 190 | |
| Phe | Asn | Phe | Leu | Arg | Lys | Lys | Leu | Phe | Phe | Met | | | | | |
| | | 195 | | | | | 200 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGCTGGTG TGATGTTTTA AAGAAAAGTT TTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|--|----|
| TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTTT | 60 |
| CCGGAG | 66 |

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KIKLY, KRISTINE K.
RUBEN, STEVEN M.
- (ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING
ENZYME LIKE APOPTOTIC PROTEASE-6
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/952,936
(B) FILING DATE: 08-MAY-1997
(C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/013,961
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p30483-2
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346169

(2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
1 5 10 15
Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
20 25 30
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
35 40 45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
50 55 60
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
65 70 75 80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
85 90 95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
100 105 110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
115 120 125
Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
130 135 140
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
145 150 155 160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
165 170 175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
180 185 190
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
195 200 205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
210 215 220
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
225 230 235 240
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
245 250 255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
260 265 270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
275 280 285 290
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
295 300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
305 310 315 320
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
325 330 335
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
340 345 350
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
355 360 365

000100100000

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Phe | Glu | Gln | Trp | Ala | His | Ser | Glu | Asp | Leu | Gln | Ser | Leu | Leu |
| 370 | | | | | | 375 | | | | | 380 | | | | |
| Leu | Arg | Val | Ala | Asn | Ala | Val | Ser | Val | Lys | Gly | Ile | Tyr | Lys | Gln | Met |
| 385 | | | | 390 | | | | | 395 | | | | | | 400 |
| Pro | Gly | Cys | Phe | Asn | Phe | Leu | Arg | Lys | Lys | Leu | Phe | Phe | Lys | Thr | Ser |
| | | | 405 | | | | | 410 | | | | | 415 | | |

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|-------------|------|
| GCCATGGACG | AAGCGGATCG | GCGGCTCCTG | CGGCGGTGCC | GGCTGCGGCT | GGTGAAGAG | 60 |
| CTGCAGGTGG | ACCAGCTCTG | GGACGTCCTG | CTGAGCCGCG | AGCTGTTTCAG | GCCCCATATG | 120 |
| ATCGAGGACA | TCCAGCGGGC | AGGCTCTGGA | TCTCGGCGGG | ATCAGGCCAG | GCAGCTGATC | 180 |
| ATAGATCTGG | AGACTCGAGG | GAGTCAGGCT | CTTCCTTTGT | TCATCTCCTG | CTTAGAGGAC | 240 |
| ACAGGCCAGG | ACATGCTGGC | TTCGTTTCTG | CGAACTAACA | GGCAAGCAGG | AAAGTTGTCTG | 300 |
| AAGCCAAACC | TAGAAAACCT | TACCCACGTG | GTGCTCAGAC | CAGAGATTCTG | CAAACCAGAG | 360 |
| GTTCTCAGAC | CGGAAACACC | CAGACCAGTG | GACATTGGTT | CTGGAGGATT | CGGTGATGTC | 420 |
| GGTGCTCTTG | AGAGTTTGAG | GGGAAATGCA | GATTTGGCTT | ACATCCTGAG | CATGGAGCCC | 480 |
| TGTGGCCACT | GCCTCATTAT | CAACRATGTG | AACCTCTGCC | GTGAGTCCGG | GCTCCGCACC | 540 |
| CGCACTGGCT | CCAACATCGA | CTGTGAGAAG | TTGCGGCGTC | GCTTCTCCTC | GCTGCATTTT | 600 |
| ATGGTGGAGG | TGAAGGGCGA | CCTGACTGCC | AAGAAAATGG | TGCTGGCTTT | GCTGGAGCTG | 660 |
| GCGCGGCAGG | ACCACGGTGC | TCTGGACTGC | TGCTGGGTGG | TCATTCTCTC | TCACGGCTGT | 720 |
| CAGGCCAGCC | ACCTGCAGTT | CCCAGGGGCT | GTCTACGGCA | CAGATGGATG | CCCTGTGTCTG | 780 |
| GTGAGAAGA | TTGTGAACAT | CTTCAATGGG | ACCAGCTGCC | CCAGCCTGGG | AGGGAAGCCC | 840 |
| AAGCTCTTTT | TCATCCAGGC | CTGTGGTGGG | GAGCAGAAAG | ACCATGGGTT | TGAGGTGGCC | 900 |
| TCCACTTCCC | CTGAAGACGA | GTCCCTGGC | AGTAACCCCG | AGCCAGATGC | CACCCCGTTC | 960 |
| CAGGAAGGTT | TGAGGACCTT | CGACCAGCTG | GACGCCATAT | CTAGTTTGCC | CACACCCAGT | 1020 |
| GACATCTTTG | TGTCCTACTC | TACTTTCCCA | GGTTTTGTTT | CCTGGAGGGA | CCCCAAGAGT | 1080 |
| GGCTCCTGGT | ACGTTGAGAC | CCTGGACGAC | ATCTTTGAGC | AGTGGGCTCA | CTCTGAAGAC | 1140 |
| CTGCAGTCCC | TCCTGCTTAG | GGTCGCTAAT | GCTGTTTCGG | TGAAAGGGAT | TTATAAACAG | 1200 |
| ATGCCTGGTT | GCTTTAATTT | CCTCCGGA | AACTTTTCT | TTAAAACATC | ATAAGGCCAG | 1260 |
| GGCCCTCAG | CCTGCCTTAT | CTTGACCCCC | AAAGCTTTCC | TGCCCCAGGC | CTGAAAGAGG | 1320 |
| CTGAGGCCCTG | GACTTTCTCTG | CAACTCAAGG | ACTTTGNAGC | CGGCACAGGG | TCTGCTCTTT | 1380 |
| CTCTGCCAGT | GACAGACAGG | CTCTTAGCAG | CTTCCAGATT | GACGACAAGT | GCTGAACAGT | 1440 |
| GGAGGAAGAG | GGACAGATGA | ATGCCGTGGA | TTGCACGTGG | NCTCTTGAGC | AGTGGCTGGT | 1500 |
| CCAGGGCTAG | TGACTTGGTG | TCCCATGATC | CCTGTGTTGG | TCTCTAGGAG | CAGGGATTAA | 1560 |
| CCTCTGCACT | ACTGACAT | | | | | 1578 |

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CTGACTGCCA AGAAAATGGT GCTGGCTTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGCT    60
CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC    120
CCAGGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTGCG TCGAAAAGAT TGTGAACATC    180
TTCAATGGGA CCAGCTGCCC CAGCCTGGGA GGGAAAGCCA AGCTCTTTT CATCCAGGCC    240
TGTGGTGGGG AGCAGAAAGA CCATGGGTTT GAGGTGGCCT CCACTTCCCC TGAAGACGAG    300
TCCCCTGGCA GTAACCCCGA GCCAGATGCC ACCCCGTTCC AGGAAGGTTT GAGGACCTTC    360
GACCAGCTGG ACGCCATATC TAGTTTGCCC ACACCCAGTG ACATCTTTGT GTCCTACTCT    420
ACTTTCCCAG GTTTTGTTC CTGGAGGGAC CCCAAGAGTG GCTCCTGGTA CGTTGAGACC    480
CTGGACGACA TCTTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG    540
GTCGCTAATG CTGTTTCGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTT    600
CTCCGGAAAA AACTTTTCTT TTAACATC ATAAGGCAG    639
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
1 3 10 15
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
20 25 30
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
35 40 45
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
50 55 60
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
65 70 75 80
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
85 90 95
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
100 105 110
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
115 120 125
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
130 135 140
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
145 150 155 160
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
165 170 175
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
180 185 190
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met
195 200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTAA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid

Gln Ala Cys Gly Gly
1 5

[illegible]